**Accuracy and Precision of Metagenomic Binning**

The requisite numerical information recommended by the Genomic Standards Consortium for metagenome-assembled genome is shown in Table X. The following approaches apply to all bins derived. Taxonomic classification was performed using the taxator-tk algorithm (). Reassembly of bins and initial co-assembly was performed using SPAdes 3.11(). The initial assembly was completed in metagenomic mode and reassembly was done for each bin in `careful` mode using the first pass contigs as `untrusted contigs` .

Contigs were binned according to their coverage & tetramer frequencies. A set of consensus bins were derived from the bins produced by the maxbin2, metabat2, and concoct algorithms. Completeness and contamination assessment were performed using the lineage workflow in CheckM. The bioinformatics pipeline from QC, to assembly, to binning, to refinement, to reassembly, and taxonomic classification was done within the metaWRAP software. Annotation was primarily completed using prokka (), but additional protein annotations were conducted using `metabolic-hmms` collection provided by the Banfield lab (), the ` dbCAN-fam-HMMs.v6` collection provided by BioEnergy Science Center of the DOE (), and the KEGG BlastKOALA and GhostKOALA annotation web service (). Within prokka, barrnap v0.8 and Aragorn v1.2 were used to call rRNA & tRNA respectively. Gene calls were performed using Prodigal and all protein sequences were generated using Translation Table 11.

1. Kanehisa, M., Sato, Y., and Morishima, K. (2016) BlastKOALA and GhostKOALA: KEGG tools for functional characterization of genome and metagenome sequences. J. Mol. Biol. 428, 726-731 (http://www.kegg.jp/ghostkoala/)